AMENDMENTS TO THE SPECIFICATION

Please insert the following heading and paragraph below the Title on page 1 of the specification:

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a 371 national stage of PCT/KR2005/000465 filed on February 19, 2005, which claims the benefit of the filing date of Korean Patent Application No. 10-2004-0011327, filed on February 2, 2004 and Korean Patent Application No. 10-2005-0013395, filed on February 18, 2005, in the Korean Intellectual Property Office.

Please replace the paragraph beginning on page 6, line 6, with the following replacement paragraph which is provided as a "Clean Version" and a "Marked-Up Version"

Clean Version

- SNP is a polymorphic base of a SNP polymorphic site. Here, A1 and A2 represent a low mass allele and a high mass allele, respectively, as a result of sequence analysis according a homogeneous MassEXTEND™ (hME) technique (SEQUENOM, Inc., San Diego California) and are optionally designated for convenience of experiments.

Marked-Up Version

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Please replace the paragraph beginning on page 11, line 16, with the following replacement paragraph which is provided as a "Clean Version" and a "Marked-Up Version"

Clean Version

In this Example, DNA samples were extracted from blood streams of a patient group consisting of 300 Korean men and women that had been diagnosed as colorectal cancer patients and had been being under treatment and a normal group consisting of 300 Korean men and women free from symptoms of colorectal cancer patient group, and occurrence frequencies of specific SNPs were evaluated. The SNPs were selected from a known database NCBI dbSNP (Single Nucleotide Polymorphism Database) or SEQUENOM RealSNP™ Assay Database. Primers hybridizing with sequences around the selected SNPs were used to assay nucleotides of SNPs in the DNA samples.

Marked-Up Version

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Please replace the paragraph beginning on page 12, line 24, with the following replacement paragraph which is provided as a "Clean Version" and a "Marked-Up Version"

Clean Version

Analysis of the nucleotides of SNPs in the amplified target DNA fragments was performed using a homogeneous MassEXTEND™ (hME) technique available from SEQUENOM, Inc., San Diego California. The principle of the MassEXTEND™ technique is as follows. First, primers (also called as "extension primers") ending immediately one base before SNPs within the target DNA fragments were designed. Then, the primers were hybridized with the target DNA fragments and DNA polymerization was initiated. At this time, a polymerization solution contained a reagent (e.g., ddTTP) terminating the polymerization immediately after the incorporation of a nucleotide complementary to a first allelic nucleotide (e.g., A allele). In this regard, when the first allele (e.g., A allele) exists in the target DNA fragments, products in which only a nucleotide (e.g., T nucleotide) complementary to the first allele extended from the primers will be obtained. On the other hand, when a second allele (e.g., G allele) exists in the target DNA fragments, a nucleotide (e.g., C nucleotide) complementary to the second allele is added to the 3'-ends of the primers and then the primers are extended until a nucleotide complementary to the closest first allele nucleotide (e.g., T nucleotide) is added. The lengths of products extended from the primers were determined by mass spectrometry. Therefore, alleles present in the target DNA fragments could be identified. Illustrative experimental conditions were as follows.

Marked-Up Version

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